bio-protocol Preprint

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Database construction

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An abbreviated version of this protocol was published in eLIFE in Apr 2015

Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity

DOI: 10.7554/eLife.06416

Detailed protocol

We use a suite of tools locally to perform database construction called pdm_utils. They're publicly available on github.
https://github.com/SEA-PHAGES/pdm_utils
The usage and structure are detailed in the docs.
https://pdm-utils.readthedocs.io/en/latest/
There's also a tool for database construction called PhamDB, which may be easier to use for the end-user who doesn't want to create a whole pipeline as in pdm_utils.
https://github.com/jglamine/phamdb

How to cite:(Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Russell, D. and Hatfull, G. (2021). Database construction. Bio-protocol Preprint. bio-protocol.org/prep1080.
2. Pope, W. H., Bowman, C. A., Russell, D. A., Jacobs-Sera, D., Asai, D. J., Cresawn, S. G., Jacobs, W. R., Hendrix, R. W., Lawrence, J. G. and Hatfull, G. F.(2015). Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. eLIFE. DOI: 10.7554/eLife.06416

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